

SEQUENCE LISTING

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5 (1) GENERAL INFORMATION:

(i) APPLICANT:

10 (A) NAME: VOLKER MITTENDORF
 (B) STREET: Institut de Biologie et Physiologie Vegetales
 (C) CITY: Batiment de Biologie
 (D) STATE: Lausanne
 (E) COUNTRY: Switzerland
 (F) POSTAL CODE (ZIP): CH-1015
 (G) TELEPHONE: (41) (21) 692-4222
 15 (H) TELEFAX: (41) (21) 692-4195

(A) NAME: YVES POIRIER
 (B) STREET: Institut de Biologie et Physiologie Vegetales
 (C) CITY: Batiment de Biologie
 20 (D) STATE: Lausanne
 (E) COUNTRY: Switzerland
 (F) POSTAL CODE (ZIP): CH-1015
 (G) TELEPHONE: (41) (21) 692-4222
 (H) TELEFAX: (41) (21) 692-4195

25 (ii) TITLE OF INVENTION: BIOSYNTHESIS OF MEDIUM CHAIN LENGTH
 POLYHYDROXYALKANOATES

30 (iii) NUMBER OF SEQUENCES: 26

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 35 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1677 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 45 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGAGTCAGA AGAACAATAA CGAGCTTCCC AAGCAAGCCG CGGAAAACAC GCTGAACCTG 60
 AATCCGGTGA TCGGCATCCG GGGCAAGGAC CTGCTCACCT CCGCGCGCAT GGTCTGCTC 120
 55 CAGGCGGTGC GCCAGCCGCT GCACAGCGCC AGGCACGTGG CGCATTTTCAG CCTGGAGCTG 180

	AAGAACGTCC	TGCTCGGCA	GTCGGAGCTA	CGCCAGGCG	ATGACGACCG	ACGCTTTTCC	240
	GATCCGGCCT	GGAGCCAGAA	TCCACTGTAC	AAGCGCTACA	TGCAGACCTA	CCTGGCCTGG	300
5	CGCAAGGAGC	TGCACAGCTG	GATCAGCCAC	AGCGACCTGT	CGCCGCAGGA	CATCAGTCGT	360
	GGCCAGTTCG	TCATCAACCT	GCTGACCGAG	GCGATGTCGC	CGACCAACAG	CCTGAGCAAC	420
10	CCGGCGGCGG	TCAAGCGCTT	CTTCGAGACC	GGCGGCAAGA	GCCTGCTGGA	CGGCCTCGGC	480
	CACCTGGCCA	AGGACCTGGT	GAACAACGGC	GGGATGCCGA	GCCAGGTGGA	CATGGACGCC	540
	TTTCGAGGTG	GCAAGAACCT	GGCCACCACC	GAGGGCGCCG	TGGTGTTCGG	CAACGACGTG	600
15	CTGGAAGTGA	TCCAGTACCG	GCCGATCACC	GAGTCGGTGC	ACGAACGCCC	GCTGCTGGTG	660
	GTGCCGCCGC	AGATCAACAA	GTTCTACGTC	TTCGACCTGT	CGCCGGACAA	GAGCCTGGCG	720
20	CGCTTCTGCC	TGCGCAACGG	CGTGCAGACC	TTCATCGTCA	GTTGGCGCAA	CCCGACCAAG	780
	TCGCAGCGCG	AATGGGGCCT	GACCACCTAT	ATCGAGGCGC	TCAAGGAGGC	CATCGAGGTA	840
	GTCCTGTCGA	TCACCGGCAG	CAAGGACCTC	AACCTCCTCG	GCGCCTGCTC	CGGCGGGATC	900
25	ACCACCGCGA	CCCTGGTCGG	CCACTACGTG	GCCAGCGGCG	AGAAGAAGGT	CAACGCCTTC	960
	ACCCAACTGG	TCAGCGTGCT	CGACTTCGAA	CTGAATACCC	AGGTCGCGCT	GTTCCGCCGAC	1020
30	GAGAAGACTC	TGGAGGCCGC	CAAGCGTCGT	TCCTACCAGT	CCGGCGTGCT	GGAGGGCAAG	1080
	GACATGGCCA	AGGTGTTTCG	CTGGATGCGC	CCCAACGACC	TGATCTGGAA	CTACTGGGTC	1140
	AACAACCTACC	TGCTCGGCAA	CCAGCCGCCG	GCGTTCGACA	TCCTCTACTG	GAACAACGAC	1200
35	ACCACGCGCC	TGCCCCCGCG	GCTGCACGGC	GAGTTCGTGC	AACTGTTCAA	GAGCAACCCG	1260
	CTGAACCGCC	CCGGCGCCCT	GGAGGTCTCC	GGCACGCCCC	TCGACCTGAA	GCAGGTGACT	1320
40	TGCGACTTCT	ACTGTGTCGC	CGGTCTGAAC	GACCACATCA	CCCCCTGGGA	GTCGTGCTAC	1380
	AAGTCGGCCA	GGCTGCTGGG	TGGCAAGTGC	GAGTTCATCC	TCTCCAACAG	CGGTCACATC	1440
	CAGAGCATCC	TCAACCCACC	GGGCAACCCC	AAGGCACGCT	TCATGACCAA	TCCGGAACTG	1500
45	CCCGCCGAGC	CCAAGGCCTG	GCTGGAACAG	GCCGGCAAGC	ACGCCGACTC	GTGGTGGTTG	1560
	CACTGGCAGC	AATGGCTGGC	CGAACGCTCC	GGCAAGACCC	GCAAGGCGCC	CGCCAGCCTG	1620
50	GGCAACAAGA	CCTATCCGGC	CGGCGAAGCC	GCGCCCGGAA	CCTACGTGCA	TGAACGA	1677

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 559 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

5 Met Ser Gln Lys Asn Asn Asn Glu Leu Pro Lys Gln Ala Ala Glu Asn
 1 5 10 15

Thr Leu Asn Leu Asn Pro Val Ile Gly Ile Arg Gly Lys Asp Leu Leu
 20 25 30

10 Thr Ser Ala Arg Met Val Leu Leu Gln Ala Val Arg Gln Pro Leu His
 35 40 45

15 Ser Ala Arg His Val Ala His Phe Ser Leu Glu Leu Lys Asn Val Leu
 50 55 60

Leu Gly Gln Ser Glu Leu Arg Pro Gly Asp Asp Asp Arg Arg Phe Ser
 65 70 75 80

20 Asp Pro Ala Trp Ser Gln Asn Pro Leu Tyr Lys Arg Tyr Met Gln Thr
 85 90 95

Tyr Leu Ala Trp Arg Lys Glu Leu His Ser Trp Ile Ser His Ser Asp
 100 105 110

25 Leu Ser Pro Gln Asp Ile Ser Arg Gly Gln Phe Val Ile Asn Leu Leu
 115 120 125

Thr Glu Ala Met Ser Pro Thr Asn Ser Leu Ser Asn Pro Ala Ala Val
 130 135 140

Lys Arg Phe Phe Glu Thr Gly Gly Lys Ser Leu Leu Asp Gly Leu Gly
 145 150 155 160

35 His Leu Ala Lys Asp Leu Val Asn Asn Gly Gly Met Pro Ser Gln Val
 165 170 175

Asp Met Asp Ala Phe Glu Val Gly Lys Asn Leu Ala Thr Thr Glu Gly
 180 185 190

40 Ala Val Val Phe Arg Asn Asp Val Leu Glu Leu Ile Gln Tyr Arg Pro
 195 200 205

Ile Thr Glu Ser Val His Glu Arg Pro Leu Leu Val Val Pro Pro Gln
 210 215 220

45 Ile Asn Lys Phe Tyr Val Phe Asp Leu Ser Pro Asp Lys Ser Leu Ala
 225 230 235 240

50 Arg Phe Cys Leu Arg Asn Gly Val Gln Thr Phe Ile Val Ser Trp Arg
 245 250 255

Asn Pro Thr Lys Ser Gln Arg Glu Trp Gly Leu Thr Thr Tyr Ile Glu
 260 265 270

55 Ala Leu Lys Glu Ala Ile Glu Val Val Leu Ser Ile Thr Gly Ser Lys

275

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285

5 Asp Leu Asn Leu Leu Gly Ala Cys Ser Gly Gly Ile Thr Thr Ala Thr
 290 295 300
 Leu Val Gly His Tyr Val Ala Ser Gly Glu Lys Lys Val Asn Ala Phe
 305 310 315 320
 10 Thr Gln Leu Val Ser Val Leu Asp Phe Glu Leu Asn Thr Gln Val Ala
 325 330 335
 Leu Phe Ala Asp Glu Lys Thr Leu Glu Ala Ala Lys Arg Arg Ser Tyr
 340 345 350
 15 Gln Ser Gly Val Leu Glu Gly Lys Asp Met Ala Lys Val Phe Ala Trp
 355 360 365
 Met Arg Pro Asn Asp Leu Ile Trp Asn Tyr Trp Val Asn Asn Tyr Leu
 370 375 380
 20 Leu Gly Asn Gln Pro Pro Ala Phe Asp Ile Leu Tyr Trp Asn Asn Asp
 385 390 395 400
 Thr Thr Arg Leu Pro Ala Ala Leu His Gly Glu Phe Val Glu Leu Phe
 405 410 415
 Lys Ser Asn Pro Leu Asn Arg Pro Gly Ala Leu Glu Val Ser Gly Thr
 420 425 430
 30 Pro Ile Asp Leu Lys Gln Val Thr Cys Asp Phe Tyr Cys Val Ala Gly
 435 440 445
 Leu Asn Asp His Ile Thr Pro Trp Glu Ser Cys Tyr Lys Ser Ala Arg
 450 455 460
 35 Leu Leu Gly Gly Lys Cys Glu Phe Ile Leu Ser Asn Ser Gly His Ile
 465 470 475 480
 Gln Ser Ile Leu Asn Pro Pro Gly Asn Pro Lys Ala Arg Phe Met Thr
 485 490 495
 Asn Pro Glu Leu Pro Ala Glu Pro Lys Ala Trp Leu Glu Gln Ala Gly
 500 505 510
 45 Lys His Ala Asp Ser Trp Trp Leu His Trp Gln Gln Trp Leu Ala Glu
 515 520 525
 Arg Ser Gly Lys Thr Arg Lys Ala Pro Ala Ser Leu Gly Asn Lys Thr
 530 535 540
 50 Tyr Pro Ala Gly Glu Ala Ala Pro Gly Thr Tyr Val His Glu Arg
 545 550 555

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1680 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

	ATGCGAGAAA AGCAGGAATC GGGTAGCGTG CCGGTGCCCC CCGAGTTCAT GAGTGCACAG	60
	AGCGCCATCG TCGGCCTGCG CGGCAAGGAC CTGCTGACGA CGGTCCGCAG CCTGGCTGTC	120
15	CACGGCCTGC GCCAGCCGCT GCACAGTGCG CGGCACCTGG TCGCCTTCGG AGGCCAGTTG	180
	GGCAAGGTGC TGCTGGGCGA CACCCTGCAC CAGCCGAACC CACAGGACGC CCGCTTCCAG	240
20	GATCCATCCT GGCGCCTCAA TCCCTTCTAC CGGCGCACCC TGCAGGCCTA CCTGGCGTGG	300
	CAGAAACAAC TGCTCGCCTG GATCGACGAA AGCAACCTGG ACTGCGACGA TCGCGCCCCG	360
	GCCCCGCTTC TCGTCGCCTT GCTCTCCGAC GCCGTGGCAC CCAGCAACAG CCTGATCAAT	420
25	CCACTGGCGT TAAAGGAACT GTTCAATACC GGCGGGATCA GCCTGCTCAA TGGCGTCCGC	480
	CACCTGCTCG AAGACCTGGT GCACAACGGC GGCATGCCCA GCCAGGTGAA CAAGACCGCC	540
30	TTCGAGATCG GTCGCAACCT CGCCACCACG CAAGGCGCGG TGGTGTTCGG CAACGAGGTG	600
	CTGGAGCTGA TCCAGTACAA GCCGCTGGGC GAGCGCCAGT ACGCCAAGCC CCTGCTGATC	660
	GTGCCGCCGC AGATCAACAA GTACTACATC TTCGACCTGT CGCCGGAAAA GAGCTTCGTC	720
35	CAGTACGCCC TGAAGAACAA CCTGCAGGTC TTCGTCATCA GTTGGCGCAA CCCCACGCC	780
	CAGCACCGCG AATGGGGCCT GAGCACCTAT GTCGAGGCCC TCGACCAGGC CATCGAGGTC	840
40	AGCCGCGAGA TCACCGGCAG CCGCAGCGTG AACCTGGCCG GCGCCTGCGC CGGCGGGCTC	900
	ACCGTAGCCG CCTTGCTCGG CCACCTGCAG GTGCGCCGGC AACTGCGCAA GGTCAGTAGC	960
	GTCACCTACC TGGTCAGCCT GCTCGACAGC CAGATGGAAA GCCCGGCGAT GCTCTTCGCC	1020
45	GACGAGCAGA CCCTGGAGAG CAGCAAGCGC CGCTCCTACC AGCATGGCGT GCTGGACGGG	1080
	CGCGACATGG CCAAGGTGTT CGCCTGGATG CGCCCCAACG ACCTGATCTG GAACTACTGG	1140
50	GTCAACAACCT ACCTGCTCGG CAGGCAGCCG CCGGCGTTCG ACATCCTCTA CTGGAACAAC	1200
	GACAACACGC GGCTGCCCCG GCGGTTCCAC GGCGAACTGC TCGACCTGTT CAAGCACAAC	1260
	CCGCTGACCC GCGCGGGCGC GCTGGAGGTC AGCGGGACCG CGGTGGACCT GGGCAAGGTG	1320
55	GCGATCGACA GCTTCCACGT CGCCGGCATC ACCGACCACA TCACGCCCTG GGACGCGGTG	1380

TATCGCTCGG CCCTCCTGCT GGGCGGCCAG CGCCGCTTCA TCCTGTCCAA CAGCGGGCAC 1440
 ATCCAGAGCA TCCTCAACCC TCCCGGAAAC CCCAAGGCTT GCTACTTCGA GAACGACAAG 1500
 5 CTGAGCAGCG ATCCACGCGC CTGGTACTAC GACGCCAAGC GCGAAGAGGG CAGCTGGTGG 1560
 CCGGTCTGGC TGGGCTGGCT GCAGGAGCGC TCGGGCGAGC TGGGCAACCC TGAATTCAAC 1620
 10 CTTGGCAGCG CCGCGCATCC GCCCCTCGAA GCGGCCCCGG GCACCTACGT GCATATACGC 1680

(2) INFORMATION FOR SEQ ID NO: 4:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 560 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Arg Glu Lys Gln Glu Ser Gly Ser Val Pro Val Pro Ala Glu Phe
 1 5 10 15
 30 Met Ser Ala Gln Ser Ala Ile Val Gly Leu Arg Gly Lys Asp Leu Leu
 20 25 30
 Thr Thr Val Arg Ser Leu Ala Val His Gly Leu Arg Gln Pro Leu His
 35 35 40 45
 Ser Ala Arg His Leu Val Ala Phe Gly Gly Gln Leu Gly Lys Val Leu
 50 55 60
 40 Leu Gly Asp Thr Leu His Gln Pro Asn Pro Gln Asp Ala Arg Phe Gln
 65 70 75 80
 Asp Pro Ser Trp Arg Leu Asn Pro Phe Tyr Arg Arg Thr Leu Gln Ala
 85 90 95
 45 Tyr Leu Ala Trp Gln Lys Gln Leu Leu Ala Trp Ile Asp Glu Ser Asn
 100 105 110
 Leu Asp Cys Asp Asp Arg Ala Arg Ala Arg Phe Leu Val Ala Leu Leu
 115 120 125
 50 Ser Asp Ala Val Ala Pro Ser Asn Ser Leu Ile Asn Pro Leu Ala Leu
 130 135 140
 55 Lys Glu Leu Phe Asn Thr Gly Gly Ile Ser Leu Leu Asn Gly Val Arg
 145 150 155 160

002250-4233550

	His Leu Leu	Asp Leu Val	His Asn Gly Gly Met	Pro Ser Gln Val
		165	170	175
5	Asn Lys Thr Ala Phe Glu Ile Gly Arg Asn Leu Ala Thr Thr Gln Gly	180	185	190
	Ala Val Val Phe Arg Asn Glu Val Leu Glu Leu Ile Gln Tyr Lys Pro	195	200	205
10	Leu Gly Glu Arg Gln Tyr Ala Lys Pro Leu Leu Ile Val Pro Pro Gln	210	215	220
	Ile Asn Lys Tyr Tyr Ile Phe Asp Leu Ser Pro Glu Lys Ser Phe Val	225	230	235
15	Gln Tyr Ala Leu Lys Asn Asn Leu Gln Val Phe Val Ile Ser Trp Arg	245	250	255
	Asn Pro Asp Ala Gln His Arg Glu Trp Gly Leu Ser Thr Tyr Val Glu	260	265	270
20	Ala Leu Asp Gln Ala Ile Glu Val Ser Arg Glu Ile Thr Gly Ser Arg	275	280	285
	Ser Val Asn Leu Ala Gly Ala Cys Ala Gly Gly Leu Thr Val Ala Ala	290	295	300
	Leu Leu Gly His Leu Gln Val Arg Arg Gln Leu Arg Lys Val Ser Ser	305	310	315
30	Val Thr Tyr Leu Val Ser Leu Leu Asp Ser Gln Met Glu Ser Pro Ala	325	330	335
	Met Leu Phe Ala Asp Glu Gln Thr Leu Glu Ser Ser Lys Arg Arg Ser	340	345	350
35	Tyr Gln His Gly Val Leu Asp Gly Arg Asp Met Ala Lys Val Phe Ala	355	360	365
	Trp Met Arg Pro Asn Asp Leu Ile Trp Asn Tyr Trp Val Asn Asn Tyr	370	375	380
	Leu Leu Gly Arg Gln Pro Pro Ala Phe Asp Ile Leu Tyr Trp Asn Asn	385	390	395
45	Asp Asn Thr Arg Leu Pro Ala Ala Phe His Gly Glu Leu Leu Asp Leu	405	410	415
	Phe Lys His Asn Pro Leu Thr Arg Pro Gly Ala Leu Glu Val Ser Gly	420	425	430
50	Thr Ala Val Asp Leu Gly Lys Val Ala Ile Asp Ser Phe His Val Ala	435	440	445
	Gly Ile Thr Asp His Ile Thr Pro Trp Asp Ala Val Tyr Arg Ser Ala	450	455	460

Leu Leu Leu Gly Gly Gln Arg Arg Phe Ile Leu Ser Asn Ser Gly His
465 470 475 480

Ile Gln Ser Ile Leu Asn Pro Pro Gly Asn Pro Lys Ala Cys Tyr Phe
485 490 495

Glu Asn Asp Lys Leu Ser Ser Asp Pro Arg Ala Trp Tyr Tyr Asp Ala
500 505 510

Lys Arg Glu Glu Gly Ser Trp Trp Pro Val Trp Leu Gly Trp Leu Gln
515 520 525

Glu Arg Ser Gly Glu Leu Gly Asn Pro Asp Phe Asn Leu Gly Ser Ala
530 535 540

Ala His Pro Pro Leu Glu Ala Ala Pro Gly Thr Tyr Val His Ile Arg
545 550 555 560

20

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

35 GGAGAATTCC CGATGAGCCA GAAGAACAA

29

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

50

CTGGAAGCTT TTGATCGTTC ATGCACGTA

29

(2) INFORMATION FOR SEQ ID NO: 7:

55

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GTGGAATTCA TCGTGAAAA GCAGGAATC

29

10 (2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GGCCAAGCTT TTGAGCGTAT ATGCACGTA

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(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1731 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

40 ATGGCTGCAT CTTTCTCTGT CCCCTCTATG ATCATGGAAG AGGAAGGGAG ATTTGAGGCG 60
GAAGTTGCGG AAGTGCAGAC TTGGTGGAGC TCAGAGAGGT TCAAGCTAAC AAGGCGTCCT 120
TACACGGCCC GTGACGTGGT GGCTCTACGT GGTCATCTCA AGCAAGGTTA TGCTTCGAAC 180
45 GAGATGGCTA AGAAGCTGTG GAGAACGCTC AAGAGTCACC AAGTCAACGG CACGGCGTCT 240
CGCACGTTTG GTGCCTTGGA CCCTGTTTCTG GTGACAATGA TGGCTAAACA TTTAGACACC 300
50 ATTTATGTCT CTGGTTGGCA GTGCTCGTCT ACTCACACCT CCACTAACGA GCCTGGTCCG 360
GATCTTGCTG ACTATCCATA CGATACCGTT CCTAACAAGG TCGAACATCT CTTCTTCGCT 420
CAGCAGTACC ATGACAGAAA ACAGAGGGAG GCGAGAATGA GCATGAGCAG AGAAGAAAGA 480
55 GCAAAACTC CGTTTGTGGA CTAATTGAAG CCCATCATCG CCGACGGAGG AACCGGCTTC 540

002290-4633560

	GGCGGTACCA CTGCCACCGT AAAACTCTGC AAACCTCTTCG TTGAAAGAGG AGCCGCTGGG	600
	GTCCACATCG AGGACCAGTC CTCCGTCACC AAGAAGTGTG GCCACATGGC CGGAAAAGTC	660
5	CTCGTGGCAG TCAGTGAACA CATCAACCGC CTTGTTGCGG CTCGGCTCCA GTTCGACGTG	720
	ATGGGCACAG AGACCGTCCT GGTCGCTAGA ACGGACGCGG TCGCGCCAC TCTGATCCAA	780
10	TCGAACATTG ACTCAAGGGA CCACCAGTTC ATCCTCGGTG TACTAATCCC AAACCTTAGA	840
	GGCAAGAGTT TGTCTCGCT TCTGGCCGAG GGAATGGCTG TAGGCAATAA TGGTCCAGCG	900
	TTGCAAGCGA TTGAGGATCA ATGGCTTAGC TCAGCTCGTC TCATGACTTT CTCGGACGCT	960
15	GTCGTGGAGG CTCTCAAGCG CATGAACCTA AGTGAGAATG AGAAGAGCCG GAGAGTGACC	1020
	GAGTGGCTAA TCCATGCAAG GTACGAGAAC TGCCTTTCAA ACGAGCAAGG CCGAGAATTA	1080
20	GCAGCAAAAC TCGGTGTGAC TGATCTTTTC TGGGACTGGG ACTTGCCCAG AACCAGAGAA	1140
	GGATTCTACC GGTTCOAAGG CTCGGTCACA GCAGCCGTGG TCCGTGGCTG GGCCTTTGCA	1200
	CAGATAGCTG ATCTCATCTG GATGGAAACC GCAAGCCCTG ACCTCAACGA ATGCACCCAA	1260
25	TTCGCAGAAG GAGTCAAGTC CAAGACACCA GAGGTAATGC TCGCCTACAA CCTCTCCCCA	1320
	TCCTTCAACT GGGACGCTTC TGGTATGACG GATCAGCAGA TGATGGAGTT CATTCACGA	1380
30	ATCGCCAGGC TCGGTTATTG CTGGCAGTTT ATAACCCTTG CGGGTTTCCA TCGGATGCT	1440
	CTTGTGGTCG ATACGTTTGC AAAGGATTAC GCGAGGAGAG GGATGCTGGC TTATGTCGAG	1500
	AGGATACAGA GAGAAGAGAG GAGCAATGGG GTTGACACAT TGGCTCATCA GAAATGGTCA	1560
35	GGTGCTAATT ACTATGATCG TTATCTTAAG ACCGTCCAAG GTGGAATCTC CTCCACTGCA	1620
	GCCATGGGCA AAGGTGTTAC CGAGGAACAA TTCAAAGAGA CCTGGACGAG GCCGGGAGCT	1680
40	GCTGGAATGG GCGAAGGGAC TAGCCTTGTG GTGGCCAAGT CCAGAATGTA A	1731

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|-----------------------------|
| 45 | (A) LENGTH: 576 amino acids |
| | (B) TYPE: amino acid |
| | (C) STRANDEDNESS: |
| | (D) TOPOLOGY: linear |

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

55

Met Ala Ala Ser Phe Ser Val Pro Ser Met Ile Met Glu Glu Glu Gly

002390-4633560

	1	5	10	15
	Arg Phe Glu Ala Glu Val Ala Glu Val Gln Thr Trp Trp Ser Ser Glu			
	20	25	30	
5	Arg Phe Lys Leu Thr Arg Arg Pro Tyr Thr Ala Arg Asp Val Val Ala			
	35	40	45	
10	Leu Arg Gly His Leu Lys Gln Gly Tyr Ala Ser Asn Glu Met Ala Lys			
	50	55	60	
	Lys Leu Trp Arg Thr Leu Lys Ser His Gln Val Asn Gly Thr Ala Ser			
	65	70	75	80
15	Arg Thr Phe Gly Ala Leu Asp Pro Val Gln Val Thr Met Met Ala Lys			
	85	90	95	
	His Leu Asp Thr Ile Tyr Val Ser Gly Trp Gln Cys Ser Ser Thr His			
	100	105	110	
20	Thr Ser Thr Asn Glu Pro Gly Pro Asp Leu Ala Asp Tyr Pro Tyr Asp			
	115	120	125	
	Thr Val Pro Asn Lys Val Glu His Leu Phe Phe Ala Gln Gln Tyr His			
25	130	135	140	
	Asp Arg Lys Gln Arg Glu Ala Arg Met Ser Met Ser Arg Glu Glu Arg			
	145	150	155	160
30	Ala Lys Thr Pro Phe Val Asp Tyr Leu Lys Pro Ile Ile Ala Asp Gly			
	165	170	175	
	Gly Thr Gly Phe Gly Gly Thr Thr Ala Thr Val Lys Leu Cys Lys Leu			
	180	185	190	
35	Phe Val Glu Arg Gly Ala Ala Gly Val His Ile Glu Asp Gln Ser Ser			
	195	200	205	
	Val Thr Lys Lys Cys Gly His Met Ala Gly Lys Val Leu Val Ala Val			
40	210	215	220	
	Ser Glu His Ile Asn Arg Leu Val Ala Ala Arg Leu Gln Phe Asp Val			
	225	230	235	240
45	Met Gly Thr Glu Thr Val Leu Val Ala Arg Thr Asp Ala Val Ala Pro			
	245	250	255	
	Thr Leu Ile Gln Ser Asn Ile Asp Ser Arg Asp His Gln Phe Ile Leu			
	260	265	270	
50	Gly Val Thr Asn Pro Asn Leu Arg Gly Lys Ser Leu Ser Ser Leu Leu			
	275	280	285	
	Ala Glu Gly Met Ala Val Gly Asn Asn Gly Pro Ala Leu Gln Ala Ile			
55	290	295	300	

002230-4222550

	Glu Asp Gln	Leu Ser Ser Ala Arg Leu Met	Phe Ser Asp Ala
	305	310	315 320
5	Val Val Glu Ala	Leu Lys Arg Met Asn Leu Ser Glu Asn Glu Lys Ser	
		325 330	335
	Arg Arg Val Thr Glu Trp Leu Ile His Ala Arg Tyr Glu Asn Cys Leu		
		340 345	350
10	Ser Asn Glu Gln Gly Arg Glu Leu Ala Ala Lys Leu Gly Val Thr Asp		
		355 360	365
	Leu Phe Trp Asp Trp Asp Leu Pro Arg Thr Arg Glu Gly Phe Tyr Arg		
		370 375	380
15	Phe Gln Gly Ser Val Thr Ala Ala Val Val Arg Gly Trp Ala Phe Ala		
		385 390	395 400
	Gln Ile Ala Asp Leu Ile Trp Met Glu Thr Ala Ser Pro Asp Leu Asn		
20		405 410	415
	Glu Cys Thr Gln Phe Ala Glu Gly Val Lys Ser Lys Thr Pro Glu Val		
		420 425	430
25	Met Leu Ala Tyr Asn Leu Ser Pro Ser Phe Asn Trp Asp Ala Ser Gly		
		435 440	445
	Met Thr Asp Gln Gln Met Met Glu Phe Ile Pro Arg Ile Ala Arg Leu		
		450 455	460
30	Gly Tyr Cys Trp Gln Phe Ile Thr Leu Ala Gly Phe His Ala Asp Ala		
		465 470	475 480
	Leu Val Val Asp Thr Phe Ala Lys Asp Tyr Ala Arg Arg Gly Met Leu		
35		485 490	495
	Ala Tyr Val Glu Arg Ile Gln Arg Glu Glu Arg Ser Asn Gly Val Asp		
		500 505	510
40	Thr Leu Ala His Gln Lys Trp Ser Gly Ala Asn Tyr Tyr Asp Arg Tyr		
		515 520	525
	Leu Lys Thr Val Gln Gly Gly Ile Ser Ser Thr Ala Ala Met Gly Lys		
		530 535	540
45	Gly Val Thr Glu Glu Gln Phe Lys Glu Thr Trp Thr Arg Pro Gly Ala		
		545 550	555 560
	Ala Gly Met Gly Glu Gly Thr Ser Leu Val Val Ala Lys Ser Arg Met		
50		565 570	575

(2) INFORMATION FOR SEQ ID NO: 11:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

10

ACTGAAGCTT TGGGCAAAGG TGTTAC

26

(2) INFORMATION FOR SEQ ID NO: 12:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GTGGTCTAGA AGTTTTTCTG CGAAGATG

28

(2) INFORMATION FOR SEQ ID NO: 13:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GGCAAAGGTG TTACCGAGGA ACAATTCAAA GAGACCTGGA CGAGGCCGGG AGCTGCTGGA

60

45

ATGGGCGAAG GGACTAGCCT TGTGGTGGCC AAGTCCAGAA TG

102

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

5 Gly Lys Gly Val Thr Glu Glu Gln Phe Lys Glu Thr Trp Thr Arg Pro
1 5 10 15
Gly Ala Ala Gly Met Gly Glu Gly Thr Ser Leu Val Val Ala Lys Ser
20 25 30
10 Arg Met

(2) INFORMATION FOR SEQ ID NO: 15:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1677 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
20 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ATGAGCCAGA AGAACAATAA CGAGCTTCCC AAGCAAGCCG CGGAAAACAC GCTGAACCTG 60
AATCCGGTGA TCGGCATCCG GGGCAAGGAC CTGCTCACCT CCGCGCGCAT GGTCTTGCTC 120
30 CAGGCGGTGC GCCAGCCGCT GCACAGCGCC AGGCACGTGG CGCATTTTCAG CCTGGAGCTG 180
AAGAACGTCC TGCTCGGCCA GTCGGAGCTA CGCCCAGGCG ATGACGACCG ACGCTTTTCC 240
35 GATCCGGCCT GGAGCCAGAA TCCACTGTAC AAGCGCTACA TGCAGACCTA CCTGGCCTGG 300
CGCAAGGAGC TGCACAGCTG GATCAGCCAC AGCGACCTGT CGCCGCAGGA CATCAGTCGT 360
GGCCAGTTCG TCATCAACCT GCTGACCGAG GCGATGTCGC CGACCAACAG CCTGAGCAAC 420
40 CCGGCGGCGG TCAAGCGCTT CTTCGAGACC GGCGGCAAGA GCCTGCTGGA CGGCCTCGGC 480
CACCTGGCCA AGGACCTGGT GAACAACGGC GGGATGCCGA GCCAGGTGGA CATGGACGCC 540
45 TTCGAGGTGG GCAAGAACCT GGCCACCACC GAGGGCGCCG TGGTGTTCAG CAACGACGTG 600
CTGGAAGTGA TCCAGTACCG GCCGATCACC GAGTCGGTGC ACGAACGCCC GCTGCTGGTG 660
GTGCCGCCGC AGATCAACAA GTTCTACGTC TTCGACCTGT CGCCGGACAA GAGCCTGGCG 720
50 CGCTTCTGCC TGCGCAACGG CGTGCAGACC TTCATCGTCA GTTGGCGCAA CCCGACCAAG 780
TCGACGCGC AATGGGGCCT GACCACCTAT ATCGAGGCGC TCAAGGAGGC CATCGAGGTA 840
55 GTCCTGTCGA TCACCGGCAG CAAGGACCTC AACCTCCTCG GCGCCTGCTC CGGCGGGATC 900

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	ACCACCGCGA CCCTGCGCGG CCACTACGTG GCCAGCGGCG AGAAGAAGGT CAACGCCTTC	960
	ACCCAAGTGG TCAGCGTGCT CGACTTCGAA CTGAATACCC AGGTTCGCGCT GTTCGCCGAC	1020
5	GAGAAGACTC TGGAGGCCGC CAAGCGTCGT TCCTACCAGT CCGGCGTGCT GGAGGGCAAG	1080
	GACATGGCCA AGGTGTTTCG CTGGATGCGC CCCAACGACC TGATCTGGAA CTACTGGGTC	1140
	AACAAGTACC TGCTCGGCAA CCAGCCGCCG GCGTTCGACA TCCTCTACTG GAACAACGAC	1200
10	ACCACGCGCC TGCCCGCCGC GCTGCACGGC GAGTTCGTCG AACTGTTCAA GAGCAACCCG	1260
	CTGAACCGCC CCGGCGCCCT GGAGGTCTCC GGCACGCCCA TCGACCTGAA GCAGGTGACT	1320
15	TGCGACTTCT ACTGTGTCGC CGGTCTGAAC GACCACATCA CCCCTGGGA GTCGTGCTAC	1380
	AAGTCGGCCA GGCTGCTGGG TGGCAAGTGC GAGTTCATCC TCTCCAACAG CGGTCACATC	1440
	CAGAGCATCC TCAACCCACC GGGCAACCCC AAGGCACGCT TCATGACCAA TCCGGAAGT	1500
20	CCCGCCGAGC CCAAGGCCTG GCTGGAACAG GCCGGCAAGC ACGCCGACTC GTGGTGTTG	1560
	CACTGGCAGC AATGGCTGGC CGAACGCTCC GGCAAGACCC GCAAGGCGCC CGCCAGCCTG	1620
25	GGCAACAAGA CCTATCCGGC CGGCGAAGCC GCGCCCGGAA CCTACGTGCA TGAACGA	1677

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

40	ATGCGTGAAA AGCAGGAATC GGGTAGCGTG CCGGTGCCCC CCGAGTTCAT GAGTGCACAG	60
	AGCGCCATCG TCGGCCTGCG CGGCAAGGAC CTGCTGACGA CGGTCCGCAG CCTGGCTGTC	120
45	CACGGCCTGC GCCAGCCGCT GCACAGTGCG CGGCACCTGG TCGCCTTCGG AGGCCAGTTG	180
	GGCAAGGTGC TGCTGGGCGA CACCTTGAC CAGCCGAACC CACAGGACGC CCGCTTCCAG	240
	GATCCATCCT GCGCCTCAA TCCCTTCTAC CGGCGCACCC TGCAGGCCTA CCTGGCGTGG	300
50	CAGAAACAAC TGCTCGCCTG GATCGACGAA AGCAACCTGG ACTGCGACGA TCGCGCCCGC	360
	GCCCCGTTCC TCGTCGCCTT GCTCTCCGAC GCCGTGGCAC CCAGCAACAG CCTGATCAAT	420
55	CCACTGGCGT TAAAGGAACT GTTCAATACC GGCGGGATCA GCCTGCTCAA TGGCGTCCGC	480

CACCTGCTCG AAGAGGGT GCACAACGGC GGCATGCCCA GCCAGGAGAA CAAGACCGCC 540
 TTCGAGATCG GTCGCAACCT CGCCACCACG CAAGGCGCGG TGGTGTTCGG CAACGAGGTG 600
 5 CTGGAGCTGA TCCAGTACAA GCCGCTGGGC GAGCGCCAGT ACGCCAAGCC CCTGCTGATC 660
 GTGCCGCCGC AGATCAACAA GTACTACATC TTCGACCTGT CGCCGGAAAA GAGCTTCGTC 720
 CAGTACGCCC TGAAGAACAA CCTGCAGGTC TTCGTCATCA GTTGGCGCAA CCCCACGCC 780
 10 CAGCACCGCG AATGGGGCCT GAGCACCTAT GTCGAGGCC TCGACCAGGC CATCGAGGTC 840
 AGCCGCGAGA TCACCGGCAG CCGCAGCGTG AACCTGGCCG GCGCCTGCGC CGGCGGGCTC 900
 15 ACCGTAGCCG CCTTGCTCGG CCACCTGCAG GTGCGCCGGC AACTGCGCAA GGTCAGTAGC 960
 GTCACCTACC TGGTCAGCCT GCTCGACAGC CAGATGGAAA GCGCGGCGAT GCTCTTCGCC 1020
 GACGAGCAGA CCCTGGAGAG CAGCAAGCGC CGCTCCTACC AGCATGGCGT GCTGGACGGG 1080
 20 CGCGACATGG CCAAGGTGTT CGCCTGGATG CGCCCCAACG ACCTGATCTG GAACTACTGG 1140
 GTCAACAACCT ACCTGCTCGG CAGGCAGCCG CCGGCGTTCG ACATCCTCTA CTGGAACAAC 1200
 25 GACAACACGC GGCTGCCCCG GCGTTCCAC GGCGAACTGC TCGACCTGTT CAAGCACAAC 1260
 CCGCTGACCC GCGCGGGCGC GCTGGAGGTC AGCGGGACCG CGGTGGACCT GGGCAAGGTG 1320
 GCGATCGACA GCTTCCACGT CGCCGGCATC ACCGACCACA TCACGCCCTG GGACGCGGTG 1380
 30 TATCGCTCGG CCCTCCTGCT GGGCGGCCAG CGCCGCTTCA TCCTGTCCAA CAGCGGGCAC 1440
 ATCCAGAGCA TCCTCAACCC TCCCGGAAAC CCCAAGGCCT GCTACTTCTG GAACGACAAG 1500
 35 CTGAGCAGCG ATCCACGCGC CTGGTACTAC GACGCCAAGC GCGAAGAGGG CAGCTGGTGG 1560
 CCGGTCTGGC TGGGCTGGCT GCAGGAGCGC TCGGGCGAGC TGGGCAACCC TGAATTCAAC 1620
 40 CTTGGCAGCG CCGCGCATCC GCCCCTCGAA GCGGCCCCGG GCACCTACGT GCATATACGC 1680

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1791 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

55 ATGAGCCAGA AGAACAATAA CGAGCTTCCC AAGCAAGCCG CGGAAAACAC GCTGAACCTG 60

	AATCCGGTGA TCGGCATCCG GGGCAAGGAC CTGCTCACCT CCGCGCGCAT GGTCTGTCTC	120
	CAGGCGGTGC GCCAGCCGCT GCACAGCGCC AGGCACGTGG CGCATTTCAG CCTGGAGCTG	180
5	AAGAACGTCC TGCTCGGCCA GTCGGAGCTA CGCCCAGGCG ATGACGACCG ACGCTTTTCC	240
	GATCCGGCCT GGAGCCAGAA TCCACTGTAC AAGCGCTACA TGCAGACCTA CCTGGCCTGG	300
10	CGCAAGGAGC TGCACAGCTG GATCAGCCAC AGCGACCTGT CGCCGCAGGA CATCAGTCGT	360
	GGCCAGTTCG TCATCAACCT GCTGACCGAG GCGATGTCGC CGACCAACAG CCTGAGCAAC	420
	CCGGCGGCGG TCAAGCGCTT CTTCGAGACC GCGGCAAGA GCCTGCTGGA CGGCCTCGGC	480
15	CACCTGGCCA AGGACCTGGT GAACAACGGC GGGATGCCGA GCCAGGTGGA CATGGACGCC	540
	TTCGAGGTGG GCAAGAACCT GGCCACCACC GAGGGCGCCG TGGTGTTCG CAACGACGTG	600
20	CTGGAAGTGA TCCAGTACCG GCCGATCACC GAGTCGGTGC ACGAACGCCC GCTGCTGGTG	660
	GTGCCGCCGC AGATCAACAA GTTCTACGTC TTCGACCTGT CGCCGGACAA GAGCCTGGCG	720
	CGCTTCTGCC TGCGCAACGG CGTGCAGACC TTCATCGTCA GTTGGCGCAA CCCGACCAAG	780
25	TCGCAGCGCG AATGGGGCCT GACCACCTAT ATCGAGGCGC TCAAGGAGGC CATCGAGGTA	840
	GTCCTGTCGA TCACCGGCAG CAAGGACCTC AACCTCCTCG GCGCCTGTCT CGGCGGGATC	900
30	ACCACGCGCA CCCTGGTCGG CCACTACGTG GCCAGCGGCG AGAAGAAGGT CAACGCCTTC	960
	ACCCAAGTGG TCAGCGTGCT CGACTTCGAA CTGAATACCC AGGTCGCGCT GTTCGCCGAC	1020
	GAGAAGACTC TGGAGGCCGC CAAGCGTCGT TCCTACCAGT CCGGCGTGCT GGAGGGCAAG	1080
35	GACATGGCCA AGGTGTTCGC CTGGATGCGC CCCAACGACC TGATCTGGAA CTAAGGGTTC	1140
	AACAAGTACC TGCTCGGCAA CCAGCCGCCG GCGTTCGACA TCCTCTACTG GAACAACGAC	1200
40	ACCACGCGCC TGCCCGCCGC GCTGCACGGC GAGTTCGTCT AACTGTTCAA GAGCAACCCG	1260
	CTGAACCGCC CCGGCGCCCT GGAGGTCTCC GGCACGCCCA TCGACCTGAA GCAGGTGACT	1320
	TGCGACTTCT ACTGTGTCGC CGGTCTGAAC GACCACATCA CCCCCTGGGA GTCGTGCTAC	1380
45	AAGTCGGCCA GGCTGCTGGG TGGCAAGTGC GAGTTCATCC TCTCCAACAG CGGTCACATC	1440
	CAGAGCATCC TCAACCCACC GGGCAACCCC AAGGCACGCT TCATGACCAA TCCGGAAGTG	1500
50	CCCGCCGAGC CCAAGGCCTG GCTGGAACAG GCCGGCAAGC ACGCCGACTC GTGGTGGTTG	1560
	CACTGGCAGC AATGGCTGGC CGAACGCTCC GGCAAGACCC GCAAGGCGCC CGCCAGCCTG	1620
	GGCAACAAGA CCTATCCGGC CGGCGAAGCC GCGCCCGGAA CCTACGTGCA TGAACGATCA	1680
55	AAAGCTTTGG GCAAAGGTGT TACCGAGGAA CAATTCAAAG AGACCTGGAC GAGGCCGGGA	1740

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 597 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Ser Gln Lys Asn Asn Asn Glu Leu Pro Lys Gln Ala Ala Glu Asn
1 5 10 15

Thr Leu Asn Leu Asn Pro Val Ile Gly Ile Arg Gly Lys Asp Leu Leu
20 25 30

Thr Ser Ala Arg Met Val Leu Leu Gln Ala Val Arg Gln Pro Leu His
25 35 40 45

Ser Ala Arg His Val Ala His Phe Ser Leu Glu Leu Lys Asn Val Leu
50 55 60

Leu Gly Gln Ser Glu Leu Arg Pro Gly Asp Asp Asp Arg Arg Phe Ser
65 70 75 80

Asp Pro Ala Trp Ser Gln Asn Pro Leu Tyr Lys Arg Tyr Met Gln Thr
85 90 95

Tyr Leu Ala Trp Arg Lys Glu Leu His Ser Trp Ile Ser His Ser Asp
100 105 110

Leu Ser Pro Gln Asp Ile Ser Arg Gly Gln Phe Val Ile Asn Leu Leu
115 120 125

Thr Glu Ala Met Ser Pro Thr Asn Ser Leu Ser Asn Pro Ala Ala Val
130 135 140

Lys Arg Phe Phe Glu Thr Gly Gly Lys Ser Leu Leu Asp Gly Leu Gly
145 150 155 160

His Leu Ala Lys Asp Leu Val Asn Asn Gly Gly Met Pro Ser Gln Val
165 170 175

Asp Met Asp Ala Phe Glu Val Gly Lys Asn Leu Ala Thr Thr Glu Gly
180 185 190

Ala Val Val Phe Arg Asn Asp Val Leu Glu Leu Ile Gln Tyr Arg Pro
195 200 205

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	Ile Thr Glu	Val His Glu Arg Pro Leu Leu Val	Val Pro Pro Gln
	210	215	220
5	Ile Asn Lys Phe Tyr Val Phe Asp Leu Ser Pro Asp Lys Ser Leu Ala		
	225	230	235 240
	Arg Phe Cys Leu Arg Asn Gly Val Gln Thr Phe Ile Val Ser Trp Arg		
		245	250 255
10	Asn Pro Thr Lys Ser Gln Arg Glu Trp Gly Leu Thr Thr Tyr Ile Glu		
		260	265 270
	Ala Leu Lys Glu Ala Ile Glu Val Val Leu Ser Ile Thr Gly Ser Lys		
		275	280 285
15	Asp Leu Asn Leu Leu Gly Ala Cys Ser Gly Gly Ile Thr Thr Ala Thr		
		290	295 300
	Leu Val Gly His Tyr Val Ala Ser Gly Glu Lys Lys Val Asn Ala Phe		
20		305	310 315 320
	Thr Gln Leu Val Ser Val Leu Asp Phe Glu Leu Asn Thr Gln Val Ala		
		325	330 335
25	Leu Phe Ala Asp Glu Lys Thr Leu Glu Ala Ala Lys Arg Arg Ser Tyr		
		340	345 350
	Gln Ser Gly Val Leu Glu Gly Lys Asp Met Ala Lys Val Phe Ala Trp		
		355	360 365
30	Met Arg Pro Asn Asp Leu Ile Trp Asn Tyr Trp Val Asn Asn Tyr Leu		
		370	375 380
	Leu Gly Asn Gln Pro Pro Ala Phe Asp Ile Leu Tyr Trp Asn Asn Asp		
35		385	390 395 400
	Thr Thr Arg Leu Pro Ala Ala Leu His Gly Glu Phe Val Glu Leu Phe		
		405	410 415
40	Lys Ser Asn Pro Leu Asn Arg Pro Gly Ala Leu Glu Val Ser Gly Thr		
		420	425 430
	Pro Ile Asp Leu Lys Gln Val Thr Cys Asp Phe Tyr Cys Val Ala Gly		
		435	440 445
45	Leu Asn Asp His Ile Thr Pro Trp Glu Ser Cys Tyr Lys Ser Ala Arg		
		450	455 460
	Leu Leu Gly Gly Lys Cys Glu Phe Ile Leu Ser Asn Ser Gly His Ile		
50		465	470 475 480
	Gln Ser Ile Leu Asn Pro Pro Gly Asn Pro Lys Ala Arg Phe Met Thr		
		485	490 495
55	Asn Pro Glu Leu Pro Ala Glu Pro Lys Ala Trp Leu Glu Gln Ala Gly		
		500	505 510

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Lys His Ala Asp Ser Trp Trp Leu His Trp Gln Gln Trp Leu Ala Glu
 515 520 525
 5 Arg Ser Gly Lys Thr Arg Lys Ala Pro Ala Ser Leu Gly Asn Lys Thr
 530 535 540
 Tyr Pro Ala Gly Glu Ala Ala Pro Gly Thr Tyr Val His Glu Arg Ser
 545 550 555 560
 10 Lys Ala Leu Gly Lys Gly Val Thr Glu Glu Gln Phe Lys Glu Thr Trp
 565 570 575
 Thr Arg Pro Gly Ala Ala Gly Met Gly Glu Gly Thr Ser Leu Val Val
 15 580 585 590
 Ala Lys Ser Arg Met
 595
 20 (2) INFORMATION FOR SEQ ID NO: 19:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1794 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
 30
 35 ATGCGTGAAA AGCAGGAATC GGGTAGCGTG CCGGTGCCCCG CCGAGTTCAT GAGTGCACAG 60
 AGCGCCATCG TCGGCCTGCG CGGCAAGGAC CTGCTGACGA CCGTCCGCAG CCTGGCTGTC 120
 CACGGCCTGC GCCAGCCGCT GCACAGTGCG CGGCACCTGG TCGCCTTCGG AGGCCAGTTG 180
 40 GGCAAGGTGC TGCTGGGCGA CACCCTGCAC CAGCCGAACC CACAGGACGC CCGCTTCCAG 240
 GATCCATCCT GGCGCCTCAA TCCCTTCTAC CGGCGCACCC TGCAGGCCTA CCTGGCGTGG 300
 CAGAAACAAC TGCTCGCCTG GATCGACGAA AGCAACCTGG ACTGCGACGA TCGCGCCCGC 360
 45 GCCCGCTTCC TCGTCGCCTT GCTCTCCGAC GCCGTGGCAC CCAGCAACAG CCTGATCAAT 420
 CCACTGGCGT TAAAGGAACT GTTCAATACC GGCGGGATCA GCCTGCTCAA TGGCGTCCGC 480
 50 CACCTGCTCG AAGACCTGGT GCACAACGGC GGCATGCCCA GCCAGGTGAA CAAGACCGCC 540
 TTCGAGATCG GTCGCAACCT CGCCACCACG CAAGGCGCGG TGGTGTTCGG CAACGAGGTG 600
 CTGGAGCTGA TCCAGTACAA GCCGCTGGGC GAGCGCCAGT ACGCCAAGCC CCTGCTGATC 660
 55 GTGCCGCCGC AGATCAACAA GTACTACATC TTCGACCTGT CGCCGAAAA GAGCTTCGTC 720

CAGTACGCCC TGAAGAACAA CCTGCAGGTC TTCGTCATCA GTTGGCGCAA CCCCAGCGCC 780
 CAGCACCGCG AATGGGGCCT GAGCACCTAT GTCGAGGCCC TCGACCAGGC CATCGAGGTC 840
 5 AGCCGCGAGA TCACCGGCAG CCGCAGCGTG AACCTGGCCG GCGCCTGCGC CGGCGGGGCTC 900
 ACCGTAGCCG CCTTGCTCGG CCACCTGCAG GTGCGCCGGC AACTGCGCAA GGTCAGTAGC 960
 10 GTCACCTACC TGGTCAGCCT GCTCGACAGC CAGATGGAAA GCCCGGCGAT GCTCTTCGCC 1020
 GACGAGCAGA CCCTGGAGAG CAGCAAGCGC CGCTCCTACC AGCATGGCGT GCTGGACGGG 1080
 CGCGACATGG CCAAGGTGTT CGCCTGGATG CGCCCCAACG ACCTGATCTG GAACTACTGG 1140
 15 GTCAACAACCT ACCTGCTCGG CAGGCAGCCG CCGGCGTTCG ACATCCTCTA CTGGAACAAC 1200
 GACAACACGC GGCTGCCCCG GCGTTCAC GCGAAGTGC TCGACCTGTT CAAGCACAAC 1260
 20 CCGCTGACCC GCCCGGGCGC GCTGGAGGTC AGCGGGACCG CGGTGGACCT GGGCAAGGTG 1320
 GCGATCGACA GCTTCCACGT CGCCGGCATC ACCGACCACA TCACGCCCTG GGACGCGGTG 1380
 TATCGCTCGG CCCTCCTGCT GGGCGGCCAG CGCCGCTTCA TCCTGTCCAA CAGCGGGCAC 1440
 25 ATCCAGAGCA TCCTCAACCC TCCCGGAAAC CCCAAGGCCT GCTACTTCGA GAACGACAAG 1500
 CTGAGCAGCG ATCCACGCGC CTGGTACTAC GACGCCAAGC GCGAAGAGGG CAGCTGGTGG 1560
 30 CCGGTCTGGC TGGGCTGGCT GCAGGAGCGC TCGGGCGAGC TGGGCAACCC TGAATTCAAC 1620
 CTTGGCAGCG CCGCGCATCC GCCCCTCGAA GCGGCCCCGG GCACCTACGT GCATATACGC 1680
 TCAAAAGCTT TGGGCAAAGG TGTTACCGAG GAACAATTCA AAGAGACCTG GACGAGGCCG 1740
 35 GGAGCTGCTG GAATGGGCGA AGGGACTAGC CTTGTGGTGG CCAAGTCCAG AATG 1794

(2) INFORMATION FOR SEQ ID NO: 20:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 598 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 45 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Met Arg Glu Lys Gln Glu Ser Gly Ser Val Pro Val Pro Ala Glu Phe
 1 5 10 15
 55 Met Ser Ala Gln Ser Ala Ile Val Gly Leu Arg Gly Lys Asp Leu Leu
 20 25 30

	Thr Thr Val Arg Ser Leu Ala Val His Gly Leu Arg Gln Pro Leu His	
	35 40 45	
5	Ser Ala Arg His Leu Val Ala Phe Gly Gly Gln Leu Gly Lys Val Leu	
	50 55 60	
	Leu Gly Asp Thr Leu His Gln Pro Asn Pro Gln Asp Ala Arg Phe Gln	
	65 70 75 80	
10	Asp Pro Ser Trp Arg Leu Asn Pro Phe Tyr Arg Arg Thr Leu Gln Ala	
	85 90 95	
	Tyr Leu Ala Trp Gln Lys Gln Leu Leu Ala Trp Ile Asp Glu Ser Asn	
15	100 105 110	
	Leu Asp Cys Asp Asp Arg Ala Arg Ala Arg Phe Leu Val Ala Leu Leu	
	115 120 125	
20	Ser Asp Ala Val Ala Pro Ser Asn Ser Leu Ile Asn Pro Leu Ala Leu	
	130 135 140	
	Lys Glu Leu Phe Asn Thr Gly Gly Ile Ser Leu Leu Asn Gly Val Arg	
	145 150 155 160	
25	His Leu Leu Glu Asp Leu Val His Asn Gly Gly Met Pro Ser Gln Val	
	165 170 175	
	Asn Lys Thr Ala Phe Glu Ile Gly Arg Asn Leu Ala Thr Thr Gln Gly	
30	180 185 190	
	Ala Val Val Phe Arg Asn Glu Val Leu Glu Leu Ile Gln Tyr Lys Pro	
	195 200 205	
35	Leu Gly Glu Arg Gln Tyr Ala Lys Pro Leu Leu Ile Val Pro Pro Gln	
	210 215 220	
	Ile Asn Lys Tyr Tyr Ile Phe Asp Leu Ser Pro Glu Lys Ser Phe Val	
	225 230 235 240	
40	Gln Tyr Ala Leu Lys Asn Asn Leu Gln Val Phe Val Ile Ser Trp Arg	
	245 250 255	
	Asn Pro Asp Ala Gln His Arg Glu Trp Gly Leu Ser Thr Tyr Val Glu	
45	260 265 270	
	Ala Leu Asp Gln Ala Ile Glu Val Ser Arg Glu Ile Thr Gly Ser Arg	
	275 280 285	
50	Ser Val Asn Leu Ala Gly Ala Cys Ala Gly Gly Leu Thr Val Ala Ala	
	290 295 300	
	Leu Leu Gly His Leu Gln Val Arg Arg Gln Leu Arg Lys Val Ser Ser	
	305 310 315 320	
55	Val Thr Tyr Leu Val Ser Leu Leu Asp Ser Gln Met Glu Ser Pro Ala	

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	325	330	335
5	Met Leu Phe Ala Asp Glu Gln Thr 340	Leu Glu Ser Ser 345	Lys Arg Arg Ser 350
	Tyr Gln His Gly Val Leu Asp Gly Arg Asp Met Ala Lys Val Phe Ala 355	360	365
10	Trp Met Arg Pro Asn Asp Leu Ile Trp Asn Tyr Trp Val Asn Asn Tyr 370	375	380
	Leu Leu Gly Arg Gln Pro Pro Ala Phe Asp Ile Leu Tyr Trp Asn Asn 385	390	395 400
15	Asp Asn Thr Arg Leu Pro Ala Ala Phe His Gly Glu Leu Leu Asp Leu 405	410	415
	Phe Lys His Asn Pro Leu Thr Arg Pro Gly Ala Leu Glu Val Ser Gly 420	425	430
20	Thr Ala Val Asp Leu Gly Lys Val Ala Ile Asp Ser Phe His Val Ala 435	440	445
	Gly Ile Thr Asp His Ile Thr Pro Trp Asp Ala Val Tyr Arg Ser Ala 450	455	460
25	Leu Leu Leu Gly Gly Gln Arg Arg Phe Ile Leu Ser Asn Ser Gly His 465	470	475 480
	Ile Gln Ser Ile Leu Asn Pro Pro Gly Asn Pro Lys Ala Cys Tyr Phe 485	490	495
30	Glu Asn Asp Lys Leu Ser Ser Asp Pro Arg Ala Trp Tyr Tyr Asp Ala 500	505	510
35	Lys Arg Glu Glu Gly Ser Trp Trp Pro Val Trp Leu Gly Trp Leu Gln 515	520	525
	Glu Arg Ser Gly Glu Leu Gly Asn Pro Asp Phe Asn Leu Gly Ser Ala 530	535	540
40	Ala His Pro Pro Leu Glu Ala Ala Pro Gly Thr Tyr Val His Ile Arg 545	550	555 560
	Ser Lys Ala Leu Gly Lys Gly Val Thr Glu Glu Gln Phe Lys Glu Thr 565	570	575
45	Trp Thr Arg Pro Gly Ala Ala Gly Met Gly Glu Gly Thr Ser Leu Val 580	585	590
50	Val Ala Lys Ser Arg Met 595		

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2737 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GAATTCATGT CTCCAGTTGA TTTTAAAGAT AAAGTTGTGA TCATTACCGG TGCCGGTGGT 60
 GGT TTGGGTA AATACTACTC CCTCGAATTT GCCAAGTTGG GCGCCAAAGT CGTCGTTAAC 120
 15 GACTTGGGTG GTGCCTTGAA CGGTCAAGGT GGAAACTCCA AGGCCGCCGA CGTTGTCGTT 180
 GACGAAATTG TCAAGAACGG TGGTGTGACC GTTGCCGATT ACAACAACGT CTTGGACGGT 240
 20 GACAAGATTG TCGAAACCGC CGTCAAGAAC TTTGGTACTG TCCACGTTAT CATCAACAAT 300
 GCCGGTATCT TGAGAGATGC CTCCATGAAG AAGATGACTG AAAAAGACTA CAAATTGGTC 360
 ATTGACGTGC ACTTGAACGG TGCCTTTGCC GTCACCAAGG CTGCTTGACC ATACTTCCAA 420
 25 AAGCAAAAAT ACGGTAGAAT TGTCAACACA TCCTCCCCAG CTGGTTTGTA CGGTAACTTT 480
 GGTCAAGCCA ACTACGCCTC CGCCAAGTCT GCTTTGTTGG GATTCGCTGA AACCTTGACC 540
 30 AAGGAAGGTG CCAAATACAA CATCAAGGCC AACGCCATTG CTCCGTTGGC CAGATCAAGA 600
 ATGACTGAAT CTATCTTGCC ACCTCCAATG TTGGAAAAAT TGGGCCCTGA AAAGGTTGCC 660
 CCATTGGTCT TGTATTTGTC GTCAGCTGAA AACGAATTGA CTGGTCAATT CTTTGAAGTT 720
 35 GCTGCTGGCT TTTACGCTCA GATCAGATGG GAAAGATCCG GTGGTGTCTT GTTCAAGCCA 780
 GATCAATCCT TCACCGCTGA GGTGTGTTGCT AAGAGATTCT CTGAAATCCT TGATTATGAC 840
 40 GACTCTAGGA AGCCAGAATA CTTGAAGAAC CAATACCCAT TCATGTTGAA CGACTACGCC 900
 ACTTTGACCA ACGAAGCTAG AAAGTTGCCA GCTAACGATG CTTCTGGTGC TCCAACGTGTC 960
 TCCTTGAAGG ACAAGGTTGT TTTGATCACC GGTGCCGGTG CTGGTTTGGG TAAAGAATAC 1020
 45 GCCAAGTGGT TCGCCAAGTA CGGTGCCAAG GTTGTGTTTA ACGACTTCAA GGATGCTACC 1080
 AAGACCGTTG ACGAAATCAA AGCCGCTGGT GGTGAAGCTT GGCCAGATCA ACACGATGTT 1140
 50 GCCAAGGACT CCGAAGCTAT CATCAAGAAT GTCATTGACA AGTACGGTAC CATTGATATC 1200
 TTGGTCAACA ACGCCGGTAT CTTGAGAGAC AGATCCTTTG CCAAGATGTC CAAGCAAGAA 1260
 TGGGACTCTG TCCAACAAGT CCACTTGATT GGTACTTTCA ACTTGAGCAG ATTGGCATGG 1320
 55 CCATACTTTG TTGAAAAACA ATTTGGTAGA ATCATCAACA TTACCTCCAC CAGTGGTATC 1380

	TACGGTAACT TTGGTCAAGC CAACTACTCG TCTTCTAAGG CTGGTATCTT GGGTTTGTCC	1440
5	AAGACCATGG CCATTGAAGG TGCTAAGAAT AACATTAAGG TCAACATTGT TGCTCCACAC	1500
	GCTGAAACTG CCATGACCTT GACCATCTTC AGAGAACAAG ACAAGAACTT GTACCACGCT	1560
	GACCAAGTTG CTCCATTGTT GGTCTACTTG GGTACTGACG ATGTCCCAGT CACCGGTGAA	1620
10	ACTTCCGAAA TCGGTGGTGG TTGGATCGGT AACACCAGAT GGCAAAGAGC CAAGGGTGCT	1680
	GTCTCCCACG ACGAACACAC CACTGTTGAA TTCATCAAGG AGCACTTGAA CGAAATCACT	1740
	GACTTCACCA CTGACACTGA AAATCCAAAA TCTACCACCG AATCCTCCAT GGCTATCTTG	1800
15	TCTGCCGTTG GTGGTGATGA CGATGATGAT GACGAAGACG AAGAAGAAGA CGAAGGTGAT	1860
	GAAGAAGAAG ACGAAGAAGA CGAAGAAGAA GACGATCCAG TCTGGAGATT CGACGACAGA	1920
20	GATGTTATCT TGTACAACAT TGCCCTTGGT GCCACCACCA AGCAATTGAA GTACGTCTAC	1980
	GAAAACGACT CTGACTTCCA AGTCATTCCA ACCTTTGGTC ACTTGATCAC CTTCAACTCT	2040
	GGTAAGTCAC AAAACTCCTT TGCCAAGTTG TTGCGTAACT TCAACCCAAT GTTGTGTGTTG	2100
25	CACGGTGAAC ACTACTTGAA GGTGCACAGC TGGCCACCAC CAACCGAAGG TGAAATCAAG	2160
	ACCACTTTCG AACCAATTGC CACTACTCCA AAGGGTACCA ACGTTGTTAT TGTTCACGGT	2220
30	TCCAAATCTG TTGACAACAA GTCTGGTGAA TTGATTTACT CCAACGAAGC CACTTACTTC	2280
	ATCAGAAACT GTCAAGCCGA CAACAAGGTC TACGCTGACC GTCCAGCATT CGCCACCAAC	2340
	CAATTCTTGG CACCAAAGAG AGCCCCAGAC TACCAAGTTG ACGTTCCAGT CAGTGAAGAC	2400
35	TTGGCTGCTT TGTACCGTTT GTCTGGTGAC AGAAACCCAT TGCACATTGA TCCAAACTTT	2460
	GCTAAAGGTG CCAAGTTCCC TAAGCCAATC TTACACGGTA TGTGCACTTA TGGTTTGAGT	2520
40	GCTAAGGCTT TGATTGACAA GTTTGGTATG TTCAACGAAA TCAAGGCCAG ATTCACCGGT	2580
	ATTGTCTTCC CAGGTGAAAC CTTGAGAGTC TTGGCATGGA AGGAAAGCGA TGACACTATT	2640
	GTCTTCCAAA CTCATGTTGT TGATAGAGGT ACTATTGCCA TTAACAACGC TGCTATTAAG	2700
45	TTAGTCGGTG ACAAAGCAAA GATCTAATGA AGGATCC	2737

(2) INFORMATION FOR SEQ ID NO: 22:

- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 906 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- 55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

5 Met Ser Pro Val Asp Phe Lys Asp Lys Val Val Ile Ile Thr Gly Ala
1 5 10 15

10 Gly Gly Gly Leu Gly Lys Tyr Tyr Ser Leu Glu Phe Ala Lys Leu Gly
20 25 30

Ala Lys Val Val Val Asn Asp Leu Gly Gly Ala Leu Asn Gly Gln Gly
35 40 45

15 Gly Asn Ser Lys Ala Ala Asp Val Val Val Asp Glu Ile Val Lys Asn
50 55 60

Gly Gly Val Ala Val Ala Asp Tyr Asn Asn Val Leu Asp Gly Asp Lys
65 70 75 80

20 Ile Val Glu Thr Ala Val Lys Asn Phe Gly Thr Val His Val Ile Ile
85 90 95

25 Asn Asn Ala Gly Ile Leu Arg Asp Ala Ser Met Lys Lys Met Thr Glu
100 105 110

Lys Asp Tyr Lys Leu Val Ile Asp Val His Leu Asn Gly Ala Phe Ala
115 120 125

30 Val Thr Lys Ala Ala Trp Pro Tyr Phe Gln Lys Gln Lys Tyr Gly Arg
130 135 140

Ile Val Asn Thr Ser Ser Pro Ala Gly Leu Tyr Gly Asn Phe Gly Gln
145 150 155 160

35 Ala Asn Tyr Ala Ser Ala Lys Ser Ala Leu Leu Gly Phe Ala Glu Thr
165 170 175

40 Leu Ala Lys Glu Gly Ala Lys Tyr Asn Ile Lys Ala Asn Ala Ile Ala
180 185 190

Pro Leu Ala Arg Ser Arg Met Thr Glu Ser Ile Leu Pro Pro Pro Met
195 200 205

45 Leu Glu Lys Leu Gly Pro Glu Lys Val Ala Pro Leu Val Leu Tyr Leu
210 215 220

Ser Ser Ala Glu Asn Glu Leu Thr Gly Gln Phe Phe Glu Val Ala Ala
225 230 235 240

50 Gly Phe Tyr Ala Gln Ile Arg Trp Glu Arg Ser Gly Gly Val Leu Phe
245 250 255

Lys Pro Asp Gln Ser Phe Thr Ala Glu Val Val Ala Lys Arg Phe Ser
55 260 265 270

002290-463500

	Glu Ile Leu Asp Tyr Asp Asp Ser Arg Lys Pro Leu Tyr Leu Lys Asn	275	280	285
5	Gln Tyr Pro Phe Met Leu Asn Asp Tyr Ala Thr Leu Thr Asn Glu Ala	290	295	300
	Arg Lys Leu Pro Ala Asn Asp Ala Ser Gly Ala Pro Thr Val Ser Leu	305	310	315
10	Lys Asp Lys Val Val Leu Ile Thr Gly Ala Gly Ala Gly Leu Gly Lys	325	330	335
	Glu Tyr Ala Lys Trp Phe Ala Lys Tyr Gly Ala Lys Val Val Val Asn	340	345	350
15	Asp Phe Lys Asp Ala Thr Lys Thr Val Asp Glu Ile Lys Ala Ala Gly	355	360	365
	Gly Glu Ala Trp Pro Asp Gln His Asp Val Ala Lys Asp Ser Glu Ala	370	375	380
20	Ile Ile Lys Asn Val Ile Asp Lys Tyr Gly Thr Ile Asp Ile Leu Val	385	390	395
	Asn Asn Ala Gly Ile Leu Arg Asp Arg Ser Phe Ala Lys Met Ser Lys	405	410	415
25	Gln Glu Trp Asp Ser Val Gln Gln Val His Leu Ile Gly Thr Phe Asn	420	425	430
30	Leu Ser Arg Leu Ala Trp Pro Tyr Phe Val Glu Lys Gln Phe Gly Arg	435	440	445
	Ile Ile Asn Ile Thr Ser Thr Ser Gly Ile Tyr Gly Asn Phe Gly Gln	450	455	460
35	Ala Asn Tyr Ser Ser Ser Lys Ala Gly Ile Leu Gly Leu Ser Lys Thr	465	470	475
	Met Ala Ile Glu Gly Ala Lys Asn Asn Ile Lys Val Asn Ile Val Ala	485	490	495
40	Pro His Ala Glu Thr Ala Met Thr Leu Thr Ile Phe Arg Glu Gln Asp	500	505	510
45	Lys Asn Leu Tyr His Ala Asp Gln Val Ala Pro Leu Leu Val Tyr Leu	515	520	525
	Gly Thr Asp Asp Val Pro Val Thr Gly Glu Thr Ser Glu Ile Gly Gly	530	535	540
50	Gly Trp Ile Gly Asn Thr Arg Trp Gln Arg Ala Lys Gly Ala Val Ser	545	550	555
	His Asp Glu His Thr Thr Val Glu Phe Ile Lys Glu His Leu Asn Glu	565	570	575

	Ile Thr Asp Phe Thr Thr Asp Thr Glu Asn Pro Lys Ser Thr Thr Glu	580	585	590
5	Ser Ser Met Ala Ile Leu Ser Ala Val Gly Gly Asp Asp Asp Asp Asp	595	600	605
	Asp Glu Asp Glu Glu Glu Asp Glu Gly Asp Glu Glu Glu Asp Glu Glu	610	615	620
10	Asp Glu Glu Glu Asp Asp Pro Val Trp Arg Phe Asp Asp Arg Asp Val	625	630	635
	Ile Leu Tyr Asn Ile Ala Leu Gly Ala Thr Thr Lys Gln Leu Lys Tyr	645	650	655
15	Val Tyr Glu Asn Asp Ser Asp Phe Gln Val Ile Pro Thr Phe Gly His	660	665	670
	Leu Ile Thr Phe Asn Ser Gly Lys Ser Gln Asn Ser Phe Ala Lys Leu	675	680	685
20	Leu Arg Asn Phe Asn Pro Met Leu Leu Leu His Gly Glu His Tyr Leu	690	695	700
25	Lys Val His Ser Trp Pro Pro Pro Thr Glu Gly Glu Ile Lys Thr Thr	705	710	715
	Phe Glu Pro Ile Ala Thr Thr Pro Lys Gly Thr Asn Val Val Ile Val	725	730	735
30	His Gly Ser Lys Ser Val Asp Asn Lys Ser Gly Glu Leu Ile Tyr Ser	740	745	750
35	Asn Glu Ala Thr Tyr Phe Ile Arg Asn Cys Gln Ala Asp Asn Lys Val	755	760	765
	Tyr Ala Asp Arg Pro Ala Phe Ala Thr Asn Gln Phe Leu Ala Pro Lys	770	775	780
40	Arg Ala Pro Asp Tyr Gln Val Asp Val Pro Val Ser Glu Asp Leu Ala	785	790	795
	Ala Leu Tyr Arg Leu Ser Gly Asp Arg Asn Pro Leu His Ile Asp Pro	805	810	815
45	Asn Phe Ala Lys Gly Ala Lys Phe Pro Lys Pro Ile Leu His Gly Met	820	825	830
50	Cys Thr Tyr Gly Leu Ser Ala Lys Ala Leu Ile Asp Lys Phe Gly Met	835	840	845
	Phe Asn Glu Ile Lys Ala Arg Phe Thr Gly Ile Val Phe Pro Gly Glu	850	855	860
55	Thr Leu Arg Val Leu Ala Trp Lys Glu Ser Asp Asp Thr Ile Val Phe			

865

870

875

880

Gln Thr His Val Val Asp Arg Gly Thr Ile Ala Ile Asn Asn Ala Ala
 885 890 895

5

Ile Lys Leu Val Gly Asp Lys Ala Lys Ile
 900 905

(2) INFORMATION FOR SEQ ID NO: 23:

10

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2737 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

GGATCCATGT CTCCAGTTGA TTTTAAAGAT AAAGTTGTGA TCATTACCGG TGCCGGTGGT 60
 25 GGT TTGGGTA AATACTACTC CCTCGAATTT GCCAAGTTGG GCGCCAAAGT CGTCGTTAAC 120
 GACTTGGGTG GTGCCTTGAA CGGTCAAGGT GGAAACTCCA AGGCCGCCGA CGTTGTCGTT 180
 30 GACGAAATTG TCAAGAACGG TGGTGTGTC GTTGCCGATT ACAACAACGT CTTGGACGGT 240
 GACAAGATTG TCGAAACCGC CGTCAAGAAC TTTGGTACTG TCCACGTTAT CATCAACAAT 300
 GCCGGTATCT TGAGAGATGC CTCCATGAAG AAGATGACTG AAAAAGACTA CAAATTGGTC 360
 35 ATTGACGTGC ACTTGAACGG TGCCTTTGCC GTCACCAAGG CTGCTTG GCC ATACTTCCAA 420
 AAGCAAAAAT ACGGTAGAAT TGTC AACACA TCCTCCCCAG CTGGTTTGTA CGGTAAC TTT 480
 GGTCAAGCCA ACTACGCCTC CGCCAAGTCT GCTTTGTTGG GATTGCTGA AACCTTG GCC 540
 40 AAGGAAGGTG CCAAATACAA CATCAAGGCC AACGCCATTG CTCCGTTGGC CAGATCAAGA 600
 ATGACTGAAT CTATCTTGCC ACCTCCAATG TTGGAAAAAT TGGGCCCTGA AAAGGTTGCC 660
 45 CCATTGGTCT TGTATTTGTC GTCAGCTGAA AACGAATTGA CTGGTCAATT CTTTGAAGTT 720
 GCTGCTGGCT TTTACGCTCA GATCAGATGG GAAAGATCCG GTGGTGTCTT GTTCAAGCCA 780
 GATCAATCCT TCACCGCTGA GGTGTTGCT AAGAGATTCT CTGAAATCCT TGATTATGAC 840
 50 GACTCTAGGA AGCCAGAATA CTTGAAGAAC CAATACCCAT TCATGTTGAA CGACTACGCC 900
 ACTTTGACCA ACGAAGCTAG AAAGTTGCCA GCTAACGATG CTTCTGGTGC TCCAACTGTC 960
 55 TCCTTGAAGG ACAAGGTTGT TTTGATCACC GGTGCCGGTG CTGGTTTGGG TAAAGAATAC 1020

	GCCAAGTGGT	TCGCC	TA	CGGTGCCAAG	GTTGTTGTTA	ACGACTCAA	GGATGCTACC	1080
	AAGACCGTTG	ACGAAATCAA	AGCCGCTGGT	GGTGAAGCTT	GGCCAGATCA	ACACGATGTT	1140	
5	GCCAAGGACT	CCGAAGCTAT	CATCAAGAAT	GTCATTGACA	AGTACGGTAC	CATTGATATC	1200	
	TTGGTCAACA	ACGCCGGTAT	CTTGAGAGAC	AGATCCTTTG	CCAAGATGTC	CAAGCAAGAA	1260	
	TGGGACTCTG	TCCAACAAGT	CCACTTGATT	GGTACTTTCA	ACTTGAGCAG	ATTGGCATGG	1320	
10	CCATACTTTG	TTGAAAAACA	ATTTGGTAGA	ATCATCAACA	TTACCTCCAC	CAGTGGTATC	1380	
	TACGGTAACT	TTGGTCAAGC	CAACTACTCG	TCTTCTAAGG	CTGGTATCTT	GGGTTTGTCC	1440	
15	AAGACCATGG	CCATTGAAGG	TGCTAAGAAT	AACATTAAGG	TCAACATTGT	TGCTCCACAC	1500	
	GCTGAAACTG	CCATGACCTT	GACCATCTTC	AGAGAACAAG	ACAAGAACTT	GTACCACGCT	1560	
	GACCAAGTTG	CTCCATTGTT	GGTCTACTTG	GGTACTGACG	ATGTCCCAGT	CACCGGTGAA	1620	
20	ACTTCCGAAA	TCGGTGGTGG	TTGGATCGGT	AACACCAGAT	GGCAAAGAGC	CAAGGGTGCT	1680	
	GTCTCCCACG	ACGAACACAC	CACTGTTGAA	TTCATCAAGG	AGCACTTGAA	CGAAATCACT	1740	
25	GACTTCACCA	CTGACACTGA	AAATCCAAAA	TCTACCACCG	AATCCTCCAT	GGCTATCTTG	1800	
	TCTGCCGTTG	GTGGTGATGA	CGATGATGAT	GACGAAGACG	AAGAAGAAGA	CGAAGGTGAT	1860	
	GAAGAAGAAG	ACGAAGAAGA	CGAAGAAGAA	GACGATCCAG	TCTGGAGATT	CGACGACAGA	1920	
30	GATGTTATCT	TGTACAACAT	TGCCCTTGGT	GCCACCACCA	AGCAATTGAA	GTACGTCTAC	1980	
	GAAAACGACT	CTGACTTCCA	AGTCATTCCA	ACCTTTGGTC	ACTTGATCAC	CTTCAACTCT	2040	
35	GGTAAGTCAC	AAAACCTCCTT	TGCCAAGTTG	TTGCGTAACT	TCAACCCAAT	GTTGTTGTTG	2100	
	CACGGTGAAC	ACTACTTGAA	GGTGCACAGC	TGGCCACCAC	CAACCGAAGG	TGAAATCAAG	2160	
	ACCACTTTCG	AACCAATTGC	CACTACTCCA	AAGGGTACCA	ACGTTGTTAT	TGTTACCGGT	2220	
40	TCCAAATCTG	TTGACAACAA	GTCTGGTGAA	TTGATTTACT	CCAACGAAGC	CACTTACTTC	2280	
	ATCAGAAACT	GTCAAGCCGA	CAACAAGGTC	TACGCTGACC	GTCCAGCATT	CGCCACCAAC	2340	
45	CAATTCTTGG	CACCAAAGAG	AGCCCCAGAC	TACCAAGTTG	ACGTTCCAGT	CAGTGAAGAC	2400	
	TTGGCTGCTT	TGTACCGTTT	GTCTGGTGAC	AGAAACCCAT	TGCACATTGA	TCCAAACTTT	2460	
	GCTAAAGGTG	CCAAGTTCCC	TAAGCCAATC	TTACACGGTA	TGTGCACTTA	TGGTTTGAGT	2520	
50	GCTAAGGCTT	TGATTGACAA	GTTTGGTATG	TTCAACGAAA	TCAAGGCCAG	ATTACCGGT	2580	
	ATTGTCTTCC	CAGGTGAAAC	CTTGAGAGTC	TTGGCATGGA	AGGAAAGCGA	TGACACTATT	2640	
55	GTCTTCCAAA	CTCATGTTGT	TGATAGAGGT	ACTATTGCCA	TTAACAACGC	TGCTATTAAG	2700	

(2) INFORMATION FOR SEQ ID NO: 24:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 906 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
- 10

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Met Ser Pro Val Asp Phe Lys Asp Lys Val Val Ile Ile Thr Gly Ala
 1 5 10 15

Gly Gly Gly Leu Gly Lys Tyr Tyr Ser Leu Glu Phe Ala Lys Leu Gly
 20 25 30

Ala Lys Val Val Val Asn Asp Leu Gly Gly Ala Leu Asn Gly Gln Gly
 35 40 45

Gly Asn Ser Lys Ala Ala Asp Val Val Val Asp Glu Ile Val Lys Asn
 50 55 60

Gly Gly Val Ala Val Ala Asp Tyr Asn Asn Val Leu Asp Gly Asp Lys
 65 70 75 80

Ile Val Glu Thr Ala Val Lys Asn Phe Gly Thr Val His Val Ile Ile
 85 90 95

Asn Asn Ala Gly Ile Leu Arg Asp Ala Ser Met Lys Lys Met Thr Glu
 100 105 110

Lys Asp Tyr Lys Leu Val Ile Asp Val His Leu Asn Gly Ala Phe Ala
 115 120 125

Val Thr Lys Ala Ala Trp Pro Tyr Phe Gln Lys Gln Lys Tyr Gly Arg
 130 135 140

Ile Val Asn Thr Ser Ser Pro Ala Gly Leu Tyr Gly Asn Phe Gly Gln
 145 150 155 160

Ala Asn Tyr Ala Ser Ala Lys Ser Ala Leu Leu Gly Phe Ala Glu Thr
 165 170 175

Leu Ala Lys Glu Gly Ala Lys Tyr Asn Ile Lys Ala Asn Ala Ile Ala
 180 185 190

Pro Leu Ala Arg Ser Arg Met Thr Glu Ser Ile Leu Pro Pro Pro Met
 195 200 205

55 Leu Glu Lys Leu Gly Pro Glu Lys Val Ala Pro Leu Val Leu Tyr Leu

002290-4652550

	210		215	
	Ser Ser Ala Glu Asn Glu Leu Thr Gly Gln Phe Phe Glu Val Ala Ala			
	225		230	235 240
5	Gly Phe Tyr Ala Gln Ile Arg Trp Glu Arg Ser Gly Gly Val Leu Phe			
		245	250	255
10	Lys Pro Asp Gln Ser Phe Thr Ala Glu Val Val Ala Lys Arg Phe Ser			
		260	265	270
	Glu Ile Leu Asp Tyr Asp Asp Ser Arg Lys Pro Glu Tyr Leu Lys Asn			
		275	280	285
15	Gln Tyr Pro Phe Met Leu Asn Asp Tyr Ala Thr Leu Thr Asn Glu Ala			
		290	295	300
	Arg Lys Leu Pro Ala Asn Asp Ala Ser Gly Ala Pro Thr Val Ser Leu			
	305	310	315	320
20	Lys Asp Lys Val Val Leu Ile Thr Gly Ala Gly Ala Gly Leu Gly Lys			
		325	330	335
	Glu Tyr Ala Lys Trp Phe Ala Lys Tyr Gly Ala Lys Val Val Val Asn			
25		340	345	350
	Asp Phe Lys Asp Ala Thr Lys Thr Val Asp Glu Ile Lys Ala Ala Gly			
		355	360	365
30	Gly Glu Ala Trp Pro Asp Gln His Asp Val Ala Lys Asp Ser Glu Ala			
		370	375	380
	Ile Ile Lys Asn Val Ile Asp Lys Tyr Gly Thr Ile Asp Ile Leu Val			
35		385	390	395 400
	Asn Asn Ala Gly Ile Leu Arg Asp Arg Ser Phe Ala Lys Met Ser Lys			
		405	410	415
40	Gln Glu Trp Asp Ser Val Gln Gln Val His Leu Ile Gly Thr Phe Asn			
		420	425	430
	Leu Ser Arg Leu Ala Trp Pro Tyr Phe Val Glu Lys Gln Phe Gly Arg			
		435	440	445
45	Ile Ile Asn Ile Thr Ser Thr Ser Gly Ile Tyr Gly Asn Phe Gly Gln			
		450	455	460
	Ala Asn Tyr Ser Ser Ser Lys Ala Gly Ile Leu Gly Leu Ser Lys Thr			
	465	470	475	480
50	Met Ala Ile Glu Gly Ala Lys Asn Asn Ile Lys Val Asn Ile Val Ala			
		485	490	495
55	Pro His Ala Glu Thr Ala Met Thr Leu Thr Ile Phe Arg Glu Gln Asp			
		500	505	510

002290-452350

	Lys Asn Leu Tyr His Ala Asp Gln Val Ala Pro Leu Leu Val Tyr Leu
	515 520 525
5	Gly Thr Asp Asp Val Pro Val Thr Gly Glu Thr Ser Glu Ile Gly Gly
	530 535 540
	Gly Trp Ile Gly Asn Thr Arg Trp Gln Arg Ala Lys Gly Ala Val Ser
	545 550 555 560
10	His Asp Glu His Thr Thr Val Glu Phe Ile Lys Glu His Leu Asn Glu
	565 570 575
	Ile Thr Asp Phe Thr Thr Asp Thr Glu Asn Pro Lys Ser Thr Thr Glu
	580 585 590
15	Ser Ser Met Ala Ile Leu Ser Ala Val Gly Gly Asp Asp Asp Asp Asp
	595 600 605
	Asp Glu Asp Glu Glu Glu Asp Glu Gly Asp Glu Glu Glu Asp Glu Glu
20	610 615 620
	Asp Glu Glu Glu Asp Asp Pro Val Trp Arg Phe Asp Asp Arg Asp Val
	625 630 635 640
25	Ile Leu Tyr Asn Ile Ala Leu Gly Ala Thr Thr Lys Gln Leu Lys Tyr
	645 650 655
	Val Tyr Glu Asn Asp Ser Asp Phe Gln Val Ile Pro Thr Phe Gly His
	660 665 670
30	Leu Ile Thr Phe Asn Ser Gly Lys Ser Gln Asn Ser Phe Ala Lys Leu
	675 680 685
	Leu Arg Asn Phe Asn Pro Met Leu Leu Leu His Gly Glu His Tyr Leu
35	690 695 700
	Lys Val His Ser Trp Pro Pro Pro Thr Glu Gly Glu Ile Lys Thr Thr
	705 710 715 720
40	Phe Glu Pro Ile Ala Thr Thr Pro Lys Gly Thr Asn Val Val Ile Val
	725 730 735
	His Gly Ser Lys Ser Val Asp Asn Lys Ser Gly Glu Leu Ile Tyr Ser
	740 745 750
45	Asn Glu Ala Thr Tyr Phe Ile Arg Asn Cys Gln Ala Asp Asn Lys Val
	755 760 765
	Tyr Ala Asp Arg Pro Ala Phe Ala Thr Asn Gln Phe Leu Ala Pro Lys
50	770 775 780
	Arg Ala Pro Asp Tyr Gln Val Asp Val Pro Val Ser Glu Asp Leu Ala
	785 790 795 800
55	Ala Leu Tyr Arg Leu Ser Gly Asp Arg Asn Pro Leu His Ile Asp Pro
	805 810 815

	GCTGCTGGCT TTTACGCTCA GATCAGATGG GAAAGATCCG GTGGTGTCTT GTTCAAGCCA	780
	GATCAATCCT TCACCGCTGA GGTGTTTGCT AAGAGATTCT CTGAAATCCT TGATTATGAC	840
5	GACTCTAGGA AGCCAGAATA CTTGAAGAAC CAATACCCAT TCATGTTGAA CGACTACGCC	900
	ACTTTGACCA ACGAAGCTAG AAAGTTGCCA GCTAACGATG CTTCTGGTGC TCCAACGTGC	960
10	TCCTTGAAGG ACAAGGTTGT TTTGATCACC GGTGCCGGTG CTGGTTTGGG TAAAGAATAC	1020
	GCCAAGTGGT TCGCCAAGTA CGGTGCCAAG GTTGTTGTTA ACGACTTCAA GGATGCTACC	1080
	AAGACCGTTG ACGAAATCAA AGCCGCTGGT GGTGAAGCTT GGCCAGATCA ACACGATGTT	1140
15	GCCAAGGACT CCGAAGCTAT CATCAAGAAT GTCATTGACA AGTACGGTAC CATTGATATC	1200
	TTGGTCAACA ACGCCGGTAT CTTGAGAGAC AGATCCTTTG CCAAGATGTC CAAGCAAGAA	1260
20	TGGGACTCTG TCCAACAAGT CCACTTGATT GGTACTTTCA ACTTGAGCAG ATTGGCATGG	1320
	CCATACTTTG TTGAAAAACA ATTTGGTAGA ATCATCAACA TTACCTCCAC CAGTGGTATC	1380
	TACGGTAACT TTGGTCAAGC CAACTACTCG TCTTCTAAGG CTGGTATCTT GGGTTTGTCC	1440
25	AAGACCATGG CCATTGAAGG TGCTAAGAAT AACATTAAGG TCAACATTGT TGCTCCACAC	1500
	GCTGAAACTG CCATGACCTT GACCATCTTC AGAGAACAAG ACAAGAACTT GTACCACGCT	1560
30	GACCAAGTTG CTCCATTGTT GGTCTACTTG GGTACTGACG ATGTCCCAGT CACCGGTGAA	1620
	ACTTCCGAAA TCGGTGGTGG TTGGATCGGT AACACCAGAT GGCAAAGAGC CAAGGGTGCT	1680
	GTCTCCCACG ACGAACACAC CACTGTTGAA TTCATCAAGG AGCACTTGAA CGAAATCACT	1740
35	GACTTCACCA CTGACACTGA AAATCCAAAA TCTACCACCG AATCCTCCAT GGCTATCTTG	1800
	TCTGCCGTTG GTGGTGATGA CGATGATGAT GACGAAGACG AAGAAGAAGA CGAAGGTGAT	1860
40	GAAGAAGAAG ACGAAGAAGA CGAAGAAGAA GACGATCCAG TCTGGAGATT CGACGACAGA	1920
	GATGTTATCT TGTACAACAT TGCCCTTGGT GCCACCACCA AGCAATTGAA GTACGTCTAC	1980
	GAAAACGACT CTGACTTCCA AGTCATTCCA ACCTTTGGTC ACTTGATCAC CTTCAACTCT	2040
45	GGTAAGTCAC AAAACTCCTT TGCCAAGTTG TTGCGTAACT TCAACCCAAT GTTGTTGTTG	2100
	CACGGTGAAC ACTACTTGAA GGTGCACAGC TGGCCACCAC CAACCGAAGG TGAAATCAAG	2160
50	ACCACTTTCG AACCAATTGC CACTACTCCA AAGGGTACCA ACGTTGTTAT TGTTACGGT	2220
	TCCAAATCTG TTGACAACAA GTCTGGTGAA TTGATTTACT CCAACGAAGC CACTTACTTC	2280
	ATCAGAAACT GTCAAGCCGA CAACAAGGTC TACGCTGACC GTCCAGCATT CGCCACCAAC	2340
55	CAATTCTTGG CACCAAAGAG AGCCCCAGAC TACCAAGTTG ACGTTCCAGT CAGTGAAGAC	2400

TTGGCTGCTT TGTACCGTTT GTCTGGTGAC AGAAACCCAT TGCACATTGA TCCAAACTTT 2460
 GCTAAAGGTG CCAAGTTCCC TAAGCCAATC TTACACGGTA TGTGCACTTA TGGTTTGAGT 2520
 5 GCTAAGGCTT TGATTGACAA GTTTGGTATG TTCAACGAAA TCAAGGCCAG ATTCACCGGT 2580
 ATTGTCTTCC CAGGTGAAAC CTTGAGAGTC TTGGCATGGA AGGAAAGCGA TGACACTATT 2640
 10 GTCTTCCAAA CTCATGTTGT TGATAGAGGT ACTATTGCCA TTAACAACGC TGCTATTAAG 2700
 TTAGTCGGTG ACAAATGAAA GATCGAATGA AGGATCC 2737

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 903 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met	Ser	Pro	Val	Asp	Phe	Lys	Asp	Lys	Val	Val	Ile	Ile	Thr	Gly	Ala
1				5					10					15	
Gly	Gly	Gly	Leu	Gly	Lys	Tyr	Tyr	Ser	Leu	Glu	Phe	Ala	Lys	Leu	Gly
			20					25					30		
Ala	Lys	Val	Val	Val	Asn	Asp	Leu	Gly	Gly	Ala	Leu	Asn	Gly	Gln	Gly
		35					40					45			
Gly	Asn	Ser	Lys	Ala	Ala	Asp	Val	Val	Val	Asp	Glu	Ile	Val	Lys	Asn
	50					55					60				
Gly	Gly	Val	Ala	Val	Ala	Asp	Tyr	Asn	Asn	Val	Leu	Asp	Gly	Asp	Lys
	65				70					75					80
Ile	Val	Glu	Thr	Ala	Val	Lys	Asn	Phe	Gly	Thr	Val	His	Val	Ile	Ile
				85					90					95	
Asn	Asn	Ala	Gly	Ile	Leu	Arg	Asp	Ala	Ser	Met	Lys	Lys	Met	Thr	Glu
			100					105					110		
Lys	Asp	Tyr	Lys	Leu	Val	Ile	Asp	Val	His	Leu	Asn	Gly	Ala	Phe	Ala
		115					120					125			
Val	Thr	Lys	Ala	Ala	Trp	Pro	Tyr	Phe	Gln	Lys	Gln	Lys	Tyr	Gly	Arg
		130				135					140				
Ile	Val	Asn	Thr	Ser	Ser	Pro	Ala	Gly	Leu	Tyr	Gly	Asn	Phe	Gly	Gln
	145				150					155					160

455

[illegible]

Asn Glu Ala Thr Tyr Phe Ile Arg Asn Cys Gln Ala Asp Asn Lys Val
755 760 765

Tyr Ala Asp Arg Pro Ala Phe Ala Thr Asn Gln Phe Leu Ala Pro Lys
770 775 780

Arg Ala Pro Asp Tyr Gln Val Asp Val Pro Val Ser Glu Asp Leu Ala
785 790 795 800

Ala Leu Tyr Arg Leu Ser Gly Asp Arg Asn Pro Leu His Ile Asp Pro
805 810 815

Asn Phe Ala Lys Gly Ala Lys Phe Pro Lys Pro Ile Leu His Gly Met
820 825 830

Cys Thr Tyr Gly Leu Ser Ala Lys Ala Leu Ile Asp Lys Phe Gly Met
835 840 845

Phe Asn Glu Ile Lys Ala Arg Phe Thr Gly Ile Val Phe Pro Gly Glu
850 855 860

Thr Leu Arg Val Leu Ala Trp Lys Glu Ser Asp Asp Thr Ile Val Phe
865 870 875 880

Gln Thr His Val Val Asp Arg Gly Thr Ile Ala Ile Asn Asn Ala Ala
885 890 895

Ile Lys Leu Val Gly Asp Lys
900

[illegible]